Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application. Insertions are indicated by underscoring. Deletions are indicated by strikethrough typeface or by double brackets.

Listing of Claims:

Claims 1-56 (canceled)

57. (New) A method of identifying disease specific polymorphisms comprising: screening non-coding nucleotide sequence selected from the group consisting of non-coding nucleotide sequence three kilobases upstream of the 5' start site of protein encoding sequences and non-coding intergenomic sequences, for polymorphisms.

58. (New) The method of claim 57 wherein the protein encoding sequences are associated with a disease or disorder.

59. (New) The method of claim 57 further comprising comparing transcription factor clusters in the sequences and identifying single nucleotide polymorphisms within these clusters.

60. (New) The method of claim 57 comprising screening for Alu sequences in the non-coding sequences.

61. (New) The method of claim 60 wherein the Alu sequences form tRNA like structures.

62. (New) The method of claim 57 comprising identifying single nucleotide polymorphisms in the promoter region of a protein encoding sequence.

63. (New) The method of claim 58 comprising identifying the disease or disorder associated gene that is regulated by the single nucleotide polymorphisms harboring sequence and deducing that the gene product or an abnormal level of the product.

64. (New) The method of claim 57 wherein the analysis is carried out with the sequences available in publically available databases.

65. (New) The method of claim 64 wherein the sequences are associated with genes associated with hypertension and endocrinology.

66. (New) The method of claim 64 wherein the sequences contain single nucleotide polymorphisms in the promoter regions.

67. (New) A microarray or chip comprising a plurality of non-coding nucleotide sequences selected from the group consisting of non-coding nucleotide sequence three kilobases upstream of the 5' start site of protein encoding sequences and non-coding intergenomic sequences, wherein the nucleotide sequences comprise polymorphisms.

68. (New) The microarray of claim 67 wherein the protein encoding sequences are associated with a disease or disorder.

69. (New) The microarray of claim 67 wherein the nucleotide sequences comprise transcription factor clusters.

70. (New) The microarray of claim 69 wherein the transcription factor clusters comprise single nucleotide polymorphisms.

71. (New) The microarray of claim 67 wherein the sequences comprise Alu sequences in the non-coding sequences.

72. (New) The microarray of claim 71 wherein the Alu sequences form tRNA like structures.

73. (New) The microarray of claim 67 comprising protein encoding sequences comprising single nucleotide polymorphisms in the promoter region of a protein encoding sequence.

74. (New) The microarray of claim 67 comprising sequences known to be associated with a disease or disorder.

75. (New) The microarray of claim 67 comprising control sequences not associated with a disease or disorder.